## FOR OFFICIAL USE ONL....

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U.S. DEPARTMENT OF COMMERCE

SEARCH REQUEST FORM Requester's Full Name: Examiner # (Mandatory): Art Unit \_\_\_\_\_ Location (Bldg/Room#): \_\_\_\_/0EO Phone (circle 305 306 308) Results Format Preferred (circle): PAPER DISK E-MAIL Serial Number: \_\_\_\_ Title of Invention \_\_\_\_\_ Inventors (please provide full names): Earliest Priority Date: Keywords (include any known synonyms registry numbers, explanation of initialisms): Search Topic: Please write detailed statement of the search topic, and the concept of the invention. Describe as specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. You may include a copy of the abstract and the broadcast or most relevant claim(s). STAFF USE ONLY Type of Search Vendors (include cost where applicable) \_\_\_ STN Searcher Phone #: N.A. Sequence A.A. Sequence Questel/Orbit Searcher Location: \_\_\_\_ Structure (#) \_\_\_\_ Lexis/Nexis Date Picked Up: \_ Bibliographic \_\_\_\_ WWW/Internet Date Completed :\_\_\_ \_ Litigation 1 MP, Configure In-house sequence systems (list) 'Clerical Prep Time: \_\_ Terminal Time: Fulltext Dialog Number of Databases:\_ Procurement Dr. Link Other Westlaw Other (specify)

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 5, 1999, 07:26:47; Search time 36.08 Seconds (without alignments) 281.351 Million cell updates/sec

US-09-037-460-2 918 1 MKSVLLLTTLLVPAHLVAAW......EVVKENAAGSPVMRKWLNPR 184 Title: Perfect score: Sequence:

PAM150 Scoring table: 180763 seqs, 55169189 residues Searched:

Database :

SPTREMBL, 8:\*

1: sp\_fungi:\*
3: sp\_human:\*
4: sp\_naumal:\*
5: sp\_mhc:\*
6: sp\_organelle:\*
7: sp\_phage:\*
7: sp\_phage:\*
9: sp\_bacteria:\*
10: sp\_rodent:\*
11: sp\_virus:\*
12: sp\_vertebrate:\*
13: sp\_unclassified:\*
14: sp\_archea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q15330 homo sapien			-	063404 rattus norv		рошо	homod	ошоц	xenc	w	ഗ	073791 brachydanio			O88812 mile miscini)	P70570 rattus norv		_	090656 0911115 0911	O16270 homo santon	043666 triticum ae		P91904 caenorhabdi		093518 gloyding ha	gacycrus	homod	homo
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## ALIGNMENTS

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184 AA.

PRT;

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RESULT 2 P97682 ID P97682 AC P97682;

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                                                                                                                    RATTUS NORVEGICUS (RAT).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RGETCYRTVSGMDGMKCGPGLRCQPSNGEDPFGEEFGICKDCPYGTFGMDCRETCNCQSG 120
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.0%; Score 698; DB 10; Length 1 Best Local Similarity 74.1%; Pred. No. 4.4e-69; Matches 137; Conservative 24; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE DAWLEY; TISSUE-PINEAL GLAND;
WANG X., BROWNSTEIN M.J., YOUNG W.S.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U8018; G1750198; -
SEQUENCE 184 AA; 20075 WW; 3457564C CRC32.
CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                      184 AA; 20075 MW; 3457564C CRC32;
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STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
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Matches 37; Conservative
   01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
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180 WLNPR 184
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092743;
01-FEB-1997 (TREMBLEEL. 02, CREATED)
01-FEB-1997 (TREMBLEEL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST ANNOTATION UPDATE)
NOVEL SERIME PROTEASE.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CLONE REM4) ORF (FRAGMENT).
RATTUS NORVEGIOUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MORINAE; RATTUS.
                       52 --GCCRVCAAGRGETCYRTVSGMDGMKCGPGLRCQPSNGEDPFGEEFGICK------ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VLLLTTLLVPAHLY-AAWSNNYAVDCPQHCDSSECKSSP-----RCKRTVLDDCGCCRV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASAKURA K., POGULIS R.J., PEASE L.R., RODRIGUEZ M.;
"A monoclonal autoantibody which promotes central nervous system remyelination is highly polyreactive to multiple known and novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-PLACENTA,
MEDLINE; 97131593.
ZUMBRUNN J., TRUEB B.;
Frimary structure of a putative serine protease specific for IGF-binding proteins.";
FEBS LETT. 398:187-192(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 480;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.5%; Score 123.5; DB 2;
34.0%; Pred. No. 5.8e-06;
1ve 18; Mismatches 25;
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480 AA; 51286 MW; 175BB6D9 CRC32;
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                                                                                                     729 EDCGQECPVGTFGVNCSGSCSCVGAPCHRVTGECL 763
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EMBL, 141686, 6780367; -.
PROSITE, PSO1186, EGE_2; 5.
PFAM; PF00008; EGF, 3.
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STRAIN-HOLZMAN; TISSUE-BRAIN;
MEDLINE; 96235155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS LETT. 398.187-192(1996)
EMBL, Y07921, E275186; -
PFAM, PF00050, kazal; 1.
PFAM, PF00089; LTYPS1, 1.
PFAM, PF00519; IGFBP; 1.
PFAM, PF00519; IGFBP; 1.
PROTESES; SERINE PROTEASE.
SEQUENCE 480 AA, 51286 MW
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Best Local Similarity 34.09
Matches 33; Conservative
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ACETYL LDL RECEPTOR PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                              71 GMDGMKCGPGL---RCQPSNGEDPFGEEFGICKD-CPYGTFGMDCRETCNC-QSGICDRG 125
                                                                                                                                                                                                                                                                                          21 SNNYAVDCPQHCDSSECKSSPRCKRTVLDDCGC-----C-RVCAAGR-GETCYRTVS 70
                                                                                                                                                                                                               86 SNG-------EDPFGEEFGICKDCPYGTFGMDCRETC-NCQSGICDRGTGKCL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 DIGHCQRCDPGWLGPRCEDP------CPIGIFGEDCGSICPICVQGSCDIVIGDCV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 KRTVLDDC----GCCRVCAAGR-------GETCYRTVSGMDGMKCGPGLRCQP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 96127530.
MEDLINE; 96127530.
PROBACT., SEKI N., TANAKA A., ISHIKAWA K., NOMURA N.;
Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced papalysis of cDNA clones from human cell line KG-1.",
EMEL: D63483: 04169880; --
PROSITE; PS01186; EGF_2; 6.
                                                                                                                                                             26;
                                                                                                                          Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 830;
                                                                                                                                                        40; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                12.1%; Score 111; DB 10; 28.0%; Pred. No. 6.8e-05; tive 24; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AAWSNNYAVDCPQHCD-----SECKSSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.4%; Score 113.5; DB 2; 24.4%; Pred. No. 0.00012; tive 17; Mismatches 32;
                     1
220
23231 MW; 4389BC39 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830 AA; 87460 MW; CC490A76 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 AA
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06,
                                                                                                                                                      Conservative
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043701;
01-JUN-1998 (TREMBLREL, 06
01-JUN-1998 (TREMBLREL, 06
01-NOV-1998 (TREMBLREL, 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY:
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                   220 220 220 AA;
                                                                                                                                Local Similarity
tes 35; Conserv
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Best Local Similarity
Matches 44; Conserv
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KIAA0149.
                                                                                                                                                                                                                                                                                                                                         126 TGKCL 130
                                                                                                                                                                                                                                                                                                                                                                               138 SGTCL 142
GLYCOPROTEIN.
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SEQUENCE 83
               NON_TER
NON_TER
SEQUENCE
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043701
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8
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 PGW---WGPECQQQCECVRGRCSAASGECTCPPGFRGARCELPCPAGSHGVQCAHSCGRC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 SNG--------EDPFGEEFGICKDCPYGTFGMDCRETC-NCQSGICDRGTGKCL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 DIGHCQRCDPGWLGPRCEDP------CPIGIFGEDCGSTCPICVQGSCDIVIGDCV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 KRIVLDDC----GCCRVCAAGR-------GETCYRTVSGMDGMKCGPGLRCQP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 AGRGETCYRTVSGMDGMKCGP--GLRCQPSNGEDPFGEEFGICKD-----CPYG---- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 KQLNEDCSKTQP-----CDHTKGLECNFGASSTALK---GICRAQSEGRPCEYNSRIYQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KSVLLLTTLVPAHLVAAWSNNYAVDCPQHCDSSECKSSPRCKRT---VLDDCGCCRVCA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 RALALWYTLIHLTRLALS-----TCPAACHCP--LEAPKCAPGWGLWRDGCGCCKWCA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 KHN--EPCSPDIGSCESCEPGWNGTQCQQPCLPGIFGESCEQQCP-----HCRHGEACEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                              SEQUENCE FROM N.A.
MEDLINE; 98058897.
ADACHI H., TSUJIMOTO M., ARAI H., INOUE K.;
"Expression cloning of a novel scavenger receptor from human endothelial cells.";
J. BIOL. CHEM. 272:31217-31220(1997).
EMBL: D86864; D1024977;
PROSITE: PSO1186; EGF_2; 6.
SIGNAL; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 830;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROBER FROM N.A.
MARTINERIE C., VIEGAS-PEQUIGNOT E., NGUYEN V.C., PERBAL J. CLIN. PATHOL. MOL. PATHOL. 50:130-136(1997).
EMBL: Y11307, E304665, ...
PROSITE: PS01185; CTCK_11; 1.
PROSITE: PS01185; CTCK_11; 1.
PROSITE: PS01208; VWPC; 1.
SEQUENCE 381 AA; 42025 MW; 1B18FF1A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 12.4%; Score 113.5; DB 2; Best Local Similarity 24.4%; Pred. No. 0.00012; Matches 44; Conservative 17; Mismatches 32;
                                                                                                                                                                                                                                                                                                                           ACETYL LDL RECEPTOR. 936CC3DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AAWSNNYAVDCPQHCD-----SSECKSSP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
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                                                                                                                                                                                                                                                                                                 15 PO
830 AC
87430 MW;
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06,
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Best Local Similarity 26.1%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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PFAM; PF00093; vwc; 1.
PFAM; PF00219; IGFBP; 1.
SEOUENCE 343 AA; 37966 MW; 4F7E7114 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                            106 -----TFGMDCRETCNCQSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                          101 GTVYRSGESFQSSCKYQCTCIDG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01,
08,
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08,
                                                                                                                      Query Match
Best Local Similarity 27.3%
Matches 39; Conservative
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Best Local Similarity 25.4
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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ELM1.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENCHYTRAEUS BUCHHOLZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSTEINE-RICH-PROTEIN
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138 GPSCKCEKGD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            054775;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              earthworm."
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Q24774
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ID 054775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 CRVCAAGRGETCYRTVSGMDGMKCGPGLRCQPSNGEDP-----FGEEFGIC--KDCPY- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
CONNECTIVE TISSUE GROWTH FACTOR XCTGF.
SENOPUS LAEVIS (AFRICAN LEAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KSVLLLTTLL----VPAHLVAAWSNNYAVDCPQHCDSSECKSSPRCK---RTVLDDCGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM M.S.;
PROWLES J., GENDLER S.;
PCTS8, a new member of the connective tissue growth factor family,
Interacts with the breast cancer associated mucin MUCl.";
SUBMITIED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF083500; G3462836; -.
EMBL, AF083500; G3462816; -.
EMBL, AF0835022; IGF_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; Score 109; DB 2; Length 250; 30.4%; Pred. No. 0.00013; Live 16; Mismatches 44; Indels
                                                                                                                                                                                    01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CONNECTIVE TISSUE GROWTH FACTOR-LIKE PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.

YING 2., KING M.L.;

SUBMITTED (402-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; 043524; G2342756; -.

PROSITE; PSO11185; CTCK_1; 1.

PROSITE; PSO1208; WWFC; 1.

PROSITE; PSO1208; WWFC; 1.

PROSITE; PSO1090; Cys_knot; 1.
                                                                                                                      250 AA
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                                                                                                                                                               CREATED)
                                                                                                                      PRT;
                                                                                                                                                               08,
    109 NGESFQPNCKHQCTCIDG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 -- GTFGMDCRETCNCQSG 120
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Matches 42; Conservative
                                                                                                                   PRELIMINARY;
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                                                                                                                                                             01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                  01-NOV-1998
01-NOV-1998
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                                                                                                                                                                                                                                         55 SKOLGELCTERDV-----CDPHKGLFCD-----FGSRVNRKIGVCTAREGAPCVFG 100
                                                    Gaps
                                                                                                                                                                                               58 AAGRGETCY-RIVSGMDGMKCGP--GLRCQPSNGEDPFGE----EFGICKD-----CPYG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 GPGLRCQPSNGEDPFGEEFGICK-DCP-----YGTFGMDCRETCNCQSGICDRG---- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKSVLLLTTLLVPAHLVAAWSNNYAVDCPQHCDSSECKSSPRCK---RTVLDDCGCCRVC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILLUHN J., SCHMITT-WREDE H.P., GREVEN H., WUNDERLICH F.; "CDNA cloning of a cadmium-inducible mRNA encoding a novel cysteine-rich, non-metallothionein 25-kDa protein in an enchytraeid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; ANNELIDA; CLITELLATA; OLIGOCHAETA; HAPLOTAXIDA;
TUBIFICINA; ENCHYTRAEIDAE; ENCHYTRAEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 CDSSECK-----SSPRCKRIVLDDCGCCRVCAAGRGE-----TCYRIVSGMDGMKC
                                                    48;
  Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 98; DB 3; Length 251; 25.4%; Pred. No. 0.002; tive 18; Mismatches 34; Indels
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
10.9%; Score 100; DB 12; 27.3%; Pred. No. 0.0016; Live 18; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. BIOL. CHEM. 269:24688-24691(1994).
EMBL; X79344; G488803; -.
SEQUENCE 251 AA; 25000 MW; 85747E80 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 AA
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RA HASHINGTO Y. SHINDO-OKADA N., TANI M., NAGAMACHI Y., TAKEUCHI K.,
RA HASHINGTO Y. SHINDO-OKADA N., TANI M., NAGAMACHI Y., TAKEUCHI K.,
RA SHIKOZISHI T., TOWA H., YOKOTA J.;
RT Expression of the Elmi gene, a novel gene of the CCN (connective gene) family, suppresses in vivo tumor growth and metastasis of K-1735 Murine melanoma cells.";
RL J. EXP. MED. 187:289-296(1998).
BRL J. EXP. MED. 187:289-296(1998).
BRL ABOOGRE: PS01185; CTCK\_1; 1.
SQ SEQUENCE 367 AA; 40702 MW; labs35AB9 CRC32; 10; ä Burartota, metazoa; Chordata; Vertebrata; Madomalta; cuthqqta; Goddayra, Sciurocmathi; Huridae; Muriche; Bus, Gaps 82 RCOPSNGEDPFGEEFGICKD-----C----PY---GIFGMDGRETCNCQSGI--CDRGT 126 BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO). BUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA; CYPRINIDAE; RASBORINAE; DANIO. 27 DCPOHCDSSECKSSPRCK---RIVLDDCGCCRVCAAGRGETCYRIVSGMDGMKCGP--GL 81 66 YRTVSGMDGMKCGPG----- 100 Gaps 7 LITLLVPAHLVAAWSNNYAVDCPQHCDSSECKSSPRCKRIVLDDCGCCRVCAAG-RGEIC 65 39; Length 367; 65; 10.7%; Score 98.5; DB 12; Length 1116; 23.7%; Pred. No. 0.0066; tive 18; Mismatches 33; Indels 65; 10.6%; Score 97.5; DB 10; Length 3/ 28.2%; Pred. No. 0.0032; tive 15; Mismatches 35; Indels 01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
ENDOTHELIUM-SPECIFIC RECEPTOR TYROSINE KINASE TIE-2. SEQUENCE FROM N.A.
LYONS M.S., BELL B., STAINIER D., PETERS K.G.;
LYONS DEV. DYN. 0:0-0(1998).
EMBL; AF053632; G3005607; -.
SEQUENCE 1116 AA: 122361 MW; 7E60F6C5 CRC32; PRT; 1116 AA 296 WRGLSCNDACPDGYYGAGCTQKCVCAKGRCDR 327 -----KDCPYGTFGMDCRETCNCQSGICDR 124 Conservative PRELIMINARY; 36; Conservative Ouery Match Best Local Similarity Thes 35; Conserve Best Local Similarity 127 GKCL 130 155 PLCL 158 **Ouery Match** 073791; 073791 RESULT 13 073791 Matches 100 ٠۵ 셤 ò ద ò SO SO SO SE LA PARTICIO DE LA PARTICIO DEL PARTICIO DE LA PARTICIO DEL PAR õ 쉽 ò g ò

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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                820 PRRCDPCQCSGEGSLSAVCD-TVTGQCPCRQGAHGSRCDRCQPCHWGFPTCRPCQCNGHA 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 E-----TCYRTVSGMDGMKC---------GPGLRCQPSN-GEDPFGE-EFGI-- 99
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NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 POHCDSSECKS----SPRCKRIVLDDCGC------CRVCA-AGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA RES. 5:31-39(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86;
                                                                                                                                                                                             GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.6%; Score 97; DB 12; Length 1792; 23.0%; Pred. No. 0.015; tive 22; Mismatches 36; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDUTENCE FROM N.A.
LIU J., SWASDISON S., XIE W., BREWTON R.G., MAYNE R.;
WATRIX BIOL. 16.0-0(1998).
EMBL; AP038555; G2708707;
PROSITE; PS01186; EGF_2; Z.
PROSITE; PS011248; LAMININ_TYPE_EGF; 12.
DESCRIPTION OF THE PROPERTY (SO. DESCRIPTION OF PROPERTY OF THE PROPERTY OF TH
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01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
KIAAO533 PROTEIN (LAMININ ALPHA 5 CHAIN) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 93015947.
O'REAR J.J.;
A novel laminin Bl chain variant in avian eye.
J. BIOL. CHEM. 267:20555-20557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1792 AA; 195722 MW; AFFC9020 CRC32;
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SEQUENCE OF 693-1645 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 23.0%
Matches 43; Conservative
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HOMO SAPIENS (HUMA)
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SEQUENCE 17
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WEDLINE; 97415425.
WEDLINE; 97415425.
WEDLINE; 97415426.
WEDLINE U.M.;
"Tissue-specific expression of the human laminin alpha5-chain, and ampping of the gene to human chromosome 20q13.2-13.3 and to distal mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
WEDLINE; 295136; D1025389; -...
WEDLINE; 295136; D1025389; -...
PREMI; PRO01054; laminin_G; 2.
NON_TER
NON_TER
SEQUENCE 1645 AA; 178215 MW; A44DES8F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.5%; Score 96.5; DB 2; Length 1645; Best Local Similarity 30.1%; Pred. No. 0.015; Matches 28; Conservative 12; Mismatches 20; Indels 33;
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